

Measuring Protist and Fungi Taxonomic Diversity Within The CSUSM Wetland



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Introduction

- Soil microbiome analyses on eukaryotic members of the community are poorly represented.
- We measured relative abundance of protists and fungi in the CSUSM wetland across different vegetation types (riparian (R), sedge (S), lowlands(L)) to see if there were differences in taxa.
- As microbiome analysis is a new and emerging field, we sought to add information on these eukaryotes.





Results and Figures

Methods

Collected 24 soil samples from 3 vegetation types at CSUSM wetland and extracted 15 rhizosphere samples from bulk soil

Extracted DNA via ZymoBIOMICS DNA Miniprep Kit and created NGS Library Prep EZ Kit via xGEN for shotgun metagenome sequencing

Sent off for flow cell sequencing at Illumina

To classify eukaryotes, we ran Kraken 2 on the EukRibo database, subsetting Fungi and Protists only

Taxonomic tables and alpha beta diversity graphs were created and extracted using R and Excel



Fig. 1 Alpha Diversity across bulk soil sites. No significant difference under Simpson or Shannon pairwise between sites. Kruskal-Wallis pvalue<0.05 across all sites for Simpson.

Fig. 2 Beta Diversity across Lowland (L), Riparian (R), and Sedge (S) sites for bulk soil. No statistically significant differences across sites.

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Protist and Fungi Relative Abundance at Phylum Level



Discussion and Conclusion

- Fungi were not thought to be an important part of wetland soil communities
- ♦ However, we found Ascomycota was the most abundant phylum represented (Fig. 3)
- At class level (**Fig. 4**), a very abundant member was an anaerobic ciliate, Ciliophora Spirotrichea
- ♦ Most of the wetland was flooded when sampled, leading to anaerobic conditions where these ciliates would thrive
- Another member was Euglenozoa Euglenida
- ♦ A protist most commonly found in freshwater, especially when rich in organic matter, like our wetland.
- Alpha diversity (Fig. 1)

Fig. 3 Relative abundances for the different site and soil types across protist and fungi phyla. Samples designated with L is lowland, R is riparian, S is sedge, with _R referring to rhizosphere and _S referring to bulk soil.



♦ No differences in community pairwise between bulk soil sites

♦ Across sites, a statistically significant difference was discovered

Beta diversity (Fig. 2)

◊ Most dispersed in the lowland samples

♦ There were no significant differences across sites



Site and Soil Type

Ascomycota Saccharomycetes	Ascomycota Eurotiomycetes	Evosea Eumycetozoa	Chlorophyta Trebouxiophyceae
Ascomycota Dothideomycetes	Euglenozoa Euglenida	Endomyxa Phytomyxea	Ciliophora Spirotrichea
Ciliophora Oligohymenophorea	Bacillariophyta Coscinodiscophyceae	Apicomplexa Conoidasida	Ascomycota Schizosaccharomycetes
Ascomycota Sordariomycetes	Chlorophyta Ulvophyceae	Ascomycota Lecanoromycetes	Ciliophora Litostomatea
Apicomplexa Aconoidasida	Euglenozoa Kinetoplastea	Basidiomycota Pucciniomycetes	Rhodophyta Florideophyceae
Chlorophyta Chlorophyceae	Ciliophora Armophorea	Bacillariophyta Bacillariophyceae	Basidiomycota Agaricomycetes
Rhodophyta Bangiophyceae	Tubulinea Elardia	Chytridiomycota Chytridiomycetes	Basidiomycota Ustilaginomycetes



Fig. 4 Relative abundances for the different site and soil types across protist and fungi classes, including phylum designation. Samples designated with L is lowland, R is riparian, S is sedge, with _R referring to rhizosphere and _S referring to bulk soil.

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